AMENDMENTS TO THE CLAIMS

Listing of Claims:

1. (Previously presented) A process for the mutagenesis of a double-stranded polynucleotide sequence (master sequence) of n base-pairs having a (+)-strand and a complementary (-)-strand comprising the steps

(i) creating a collection of single-stranded fragments of the (+)-strand of the master sequence wherein all members of the collection have the same 5'-terminus and have a deletion in the 3'-terminus such that the collection represents (+)-strands with a length of n-1, n-2, n-3, ... nucleotides;

(ii) introducing at least one universal or degenerate nucleotide at the 3'-terminus of the (+)-strands produced in step (i);

(iii) elongating the (+)-strands produced in step (ii) to the full length of the master sequence using the (-)-strand or fragments thereof of the master sequence as a template strand for the elongation; and

(iv) synthesizing a (-)-strand by using the (+)-strand produced in step (iii) as a template strand thereby effecting mutations in the (-)-strand at the positions of the previous universal or degenerate nucleotides compared to the master sequence.

2. (Previously presented) The process of claim 1, wherein the collection of single-stranded fragments in step (i) is created by incorporating nucleotide analogs and subsequent cleavage in alkaline or acidic solution.

3. (Previously presented) The process of claim 2, wherein the nucleotide analog is an alpha-phosphothioate nucleotide and oxidative cleavage is achieved by iodine at the phosphothioate bonds.

4. (Currently amended) The process of claim 1, wherein step (ii) comprises elongating the collection of ~~single-stranded~~ single-stranded fragments produced in step (i) with at least one universal ~~nucleotide~~ or degenerate nucleotide by enzymatic or chemical methods.

5. (Previously presented) The process of claim 4, wherein terminal deoxynucleotidyl transferases or DNA polymerases or DNA/RNA ligases are used for elongation.

6. (Previously presented) The process of claim 1, wherein deoxyinosine, 3-nitropyrrole, 5-nitroindole or a nucleotide analog with promiscuous base pairing property is used as a universal nucleotide in step (ii).

7. (Previously presented) The process of claim 1, wherein N^6-methoxy-2,6-diaminopurine (K), N^6-methoxy-aminopurine (Z), hydroxylaminopurine (HAP), 2'-deoxyribonucleoside triphosphate (dyTP), 6H,8H-3,4-dihydropyrimidol [4,5-c][1,2] oxazin-7-one (P), N^4-aminocytidine, N^4-hydroxy-2'-deoxycytidine, N^4-methoxy-2'-deoxycytidine, 8-oxodeoxy-guanosine triphosphate (8-oxo-G) or a nucleotide analog with promiscuous base pairing property is used as degenerate nucleotide in step (ii).

8. (Currently amended) The process of claim 1, wherein an oligonucleotide of the general formula

$$\mathbf{p(U)_a(N)_b{*}(S)_c[TERM]}$$

with

p = 5'-phosphate or hydroxy-group or any chemical group capable of forming diester bonds

U = universal or degenerate nucleotides

a = arbitrary integral number from 0 to 10000

N = mixture of four bases (A/T/G/C (standard nucleotides))

b = arbitrary integral number from 0 to 100

* = cleavable group such as phosphothioate bonds in phosphothioate nucleotides

S = standard nucleotide or nucleotide analog

c = arbitrary integral number from 0 to 100

[TERM] = a dye terminator or any group preventing elongation of the oligonucleotide, with the proviso that a+b>0,

is used in step (ii) to introduce the at least one universal or degenerate nucleotide to the collection of single-stranded fragments created in step (i).

9. (Previously presented) The process of claim 8, wherein the oligonucleotide is designed in a way that

(a) stop codons and/or

(b) amino acids which disrupt secondary structures,

are avoided in the collection of the mutagenized polynucleotide sequences.

10. (Previously presented) The process of claim 8, wherein the oligonucleotide is designed in a way that

(a) transition mutations or

(b) transversion mutations,

are effected in the collection of the mutagenized polynucleotide sequences.

11. (Previously presented) The process of claim 8, wherein a DNA/RNA ligase is used for ligation of the oligonucleotides to the single-stranded fragments created in step (i), and wherein single-stranded fragments created in step (i) which are not ligated with the oligonucleotide are removed using an exonuclease.

12. (Previously presented) The process of claim 1, wherein the elongation in step (iii) is effected by a PCR reaction.

13. (Previously presented) The process of claim 1, wherein step (iii) comprises synthesizing a (-)-single stranded plasmid polynucleotide sequence from a double-stranded plasmid harboring the master sequence using a primer which anneals downstream of the (+)-strand of the master sequence, and annealing the (-)-single stranded-plasmid polynucleotide sequence with the (+)-strand produced in step (ii), and elongating the (+)-strand.

14. (Previously presented) The process of claim 1, wherein step (iii) comprises synthesizing a (-)-single-stranded plasmid harboring the master sequence using a primer which anneals downstream of the (+)-strand of the master sequence in the presence of uracil and standard nucleotides and after elongating the (+)-strand produced in step (ii), digesting the uracil carrying (-)-single-stranded plasmid with uracil glycosylase.

15. (Previously presented) The process of claim 1, wherein a PCR amplification is used after step (iii) in order to synthesize a (-)-strand complementary to the (+)-strand produced in step (iii), thereby effecting a double-stranded master sequence carrying mutations.